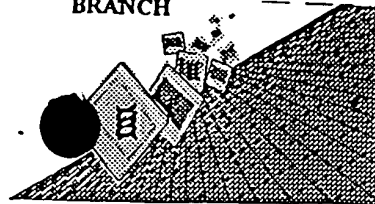


RAW SEQUENCE LISTING ERROR REPORT

BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09582397

Source: PCT09

Date Processed by STIC: 11/14/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/582397

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ✓ Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/582,397

DATE: 11/14/2001

TIME: 14:17:30

Input Set : A:\49862seq.txt

Output Set: N:\CRF3\11142001\I582397.raw

3 <110> APPLICANT: Japan Science And Technology Corporation

5 <120> TITLE OF INVENTION: Identification of Novel Substrate I-TRAF of IKK-i Kinase

7 <130> FILE REFERENCE: JA901491

C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/582,397

C--> 9 <141> CURRENT FILING DATE: 2001-10-09

E--> 9 <160> NUMBER OF SEQ ID NOS: 4

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

53 <210> SEQ ID NO: 2
 54 <211> LENGTH: 716
 55 <212> TYPE: PRT
 56 <213> ORGANISM: Human
 W--> 57 <400> SEQUENCE: 2

(1) Amino numbering may never be aligned with the right margin. Amino numbering must be under every 5th amino acid in the sequence.

58 Met Gln Ser Thr Ala Asn Tyr Leu Trp His Thr Asp Asp Leu Leu	15
59 Gly Gln Gly Ala Thr Ala Ser Val Tyr Lys Ala Arg Asn Lys Lys	30
60 Ser Gly Glu Leu Val Ala Val Lys Val Phe Asn Thr Thr Ser Tyr	45
61 Leu Arg Pro Arg Glu Val Gln Val Arg Glu Phe Glu Val Leu Arg	60
62 Lys Leu Asn His Gln Asn Ile Val Lys Leu Phe Ala Val Glu Glu	75
63 Thr Gly Gly Ser Arg Gln Lys Val Leu Val Met Glu Tyr Cys Ser	90
64 Ser Gly Ser Leu Leu Ser Val Leu Glu Ser Pro Glu Asn Ala Phe	105
65 Gly Leu Pro Glu Asp Glu Phe Leu Val Val Leu Arg Cys Val Val	120
66 Ala Gly Met Asn His Leu Arg Glu Asn Gly Ile Val His Arg Asp	135
67 Ile Lys Pro Gly Asn Ile Met Arg Leu Val Gly Glu Glu Gly Gln	150
68 Ser Ile Tyr Lys Leu Thr Asp Phe Gly Ala Ala Arg Glu Leu Asp	165
69 Asp Asp Glu Lys Phe Val Ser Val Tyr Gly Thr Glu Glu Tyr Leu	180
70 His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys Pro Gln Gln	195
71 Lys Ala Phe Gly Val Thr Val Asp Leu Trp Ser Ile Gly Val Thr	210
72 Leu Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Ile Pro Phe Gly	225
73 Gly Pro Arg Arg Asn Lys Glu Ile Met Tyr Arg Ile Thr Thr Glu	240
74 Lys Pro Ala Gly Ala Ile Ala Gly Ala Gln Arg Arg Glu Asn Gly	255
75 Pro Leu Glu Trp Ser Tyr Thr Leu Pro Ile Thr Cys Gln Leu Ser	270
76 Leu Gly Leu Gln Ser Gln Leu Val Pro Ile Leu Ala Asn Ile Leu	285
77 Glu Val Glu Gln Ala Lys Cys Trp Gly Phe Asp Gln Phe Phe Ala	300
78 Glu Thr Ser Asp Ile Leu Gln Arg Val Val Val His Val Phe Ser	315
79 Leu Ser Gln Ala Val Leu His His Ile Tyr Ile His Ala His Asn	330
80 Thr Ile Ala Ile Phe Gln Glu Ala Val His Lys Gln Thr Ser Val	345
81 Ala Pro Arg His Gln Glu Tyr Leu Phe Glu Gly His Leu Cys Val	360
82 Leu Glu Pro Ser Val Ser Ala Gln His Ile Ala His Thr Thr Ala	375
83 Ser Ser Pro Leu Thr Leu Phe Ser Thr Ala Ile Pro Lys Gly Leu	390
84 Ala Phe Arg Asp Pro Ala Leu Asp Val Pro Lys Phe Val Pro Lys	405
85 Val Asp Leu Gln Ala Asp Tyr Asn Thr Ala Lys Gly Val Leu Gly	420
86 Ala Gly Tyr Gln Ala Leu Arg Leu Ala Arg Ala Leu Leu Asp Gly	435
87 Gln Glu Leu Met Phe Arg Gly Leu His Trp Val Met Glu Val Leu	450
88 Gln Ala Thr Cys Arg Arg Thr Leu Glu Val Ala Arg Thr Ser Leu	465
89 Leu Tyr Leu Ser Ser Ser Leu Gly Thr Glu Arg Phe Ser Ser Val	480

(2) See end of sequence error

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/582,397

DATE: 11/14/2001

TIME: 14:17:30

Input Set : A:\49862seq.txt

Output Set: N:\CRF3\11142001\I582397.raw

90	Ala Gly Thr Pro Glu Ile Gln Glu Leu Lys Ala Ala Ala Glu Leu	495
91	Arg Ser Arg Leu Arg Thr Leu Ala Glu Val Leu Ser Arg Cys Ser	510
92	Gln Asn Ile Thr Glu Thr Gln Glu Ser Leu Ser Ser Leu Asn Arg	525
93	Glu Leu Val Lys Ser Arg Asp Gln Val His Glu Asp Arg Ser Ile	540
94	Gln Gln Ile Gln Cys Cys Leu Asp Lys Met Asn Phe Ile Tyr Lys	555
95	Gln Phe Lys Lys Ser Arg Met Arg Pro Gly Leu Gly Tyr Asn Glu	570
96	Glu Gln Ile His Lys Leu Asp Lys Val Asn Phe Ser His Leu Ala	585
97	Lys Arg Leu Leu Gln Val Phe Gln Glu Glu Cys Val Gln Lys Tyr	600
98	Gln Ala Ser Leu Val Thr His Gly Lys Arg Met Arg Val Val His	615
99	Glu Thr Arg Asn His Leu Arg Leu Val Gly Cys Ser Val Ala Ala	630
100	Cys Asn Thr Glu Ala Gln Gly Val Gln Glu Ser Leu Ser Lys Leu	645
101	Leu Glu Glu Leu Ser His Gln Leu Leu Gln Asp Arg Ala Lys Gly	660
102	Ala Gln Ala Ser Pro Pro Pro Ile Ala Pro Tyr Pro Ser Pro Thr	675
103	Arg Lys Asp Leu Leu Leu His Met Gln Glu Leu Cys Glu Gly Met	690
104	Lys Leu Leu Ala Ser Asp Leu Leu Asp Asn Asn Arg Ile Ile Glu	705
E--> 105	Arg Leu Asn Arg Val Pro Ala Pro Pro Asp Val ***	716

Delete
End of file
invalid
codons

align
end of line
numbers

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/582,397

DATE: 11/14/2001

TIME: 14:17:31

Input Set : A:\49862seq.txt

Output Set: N:\CRF3\11142001\I582397.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:283 W: Missing Blank Line separator, <400> field identifier
L:57 M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:252 E: No. of Seq. differs, <211>LENGTH:Input:716 Found:0 SEQ:2
L:111 M:283 W: Missing Blank Line separator, <400> field identifier
L:166 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:167 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:168 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:169 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:170 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:171 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:172 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:173 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:174 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:175 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:176 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:177 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:178 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:179 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:180 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:181 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:182 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:183 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:184 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:185 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:186 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:187 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:188 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:189 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:190 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:191 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:192 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:193 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:194 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:195 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:196 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:197 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:198 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:199 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:200 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:201 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:202 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:203 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:204 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:205 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:206 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:207 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/582,397

DATE: 11/14/2001

TIME: 14:17:31

Input Set : A:\49862seq.txt

Output Set: N:\CRF3\11142001\I582397.raw

L:208 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
 L:209 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
 L:210 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
 L:211 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
 L:212 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
 L:213 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
 L:215 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
 L:9 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (4) Counted (3)

STATISTICS SUMMARY

PATENT APPLICATION: US/09/582,397

DATE: 11/14/2001

TIME: 14:17:31

Input Set : A:\49862seq.txt

Output Set: N:\CRF3\11142001\I582397.raw

Application Serial Number: US/09/582,397

Alpha or Numeric: Numeric

Application Class:

Application File Date: 10-09-2001

Art Unit: PCT09

Software Application:

Total Number of Sequences: 3

Total Nucleotides: 5064

Total Amino Acids: 0

Number of Errors: 2

Number of Warnings: 52

Number of Corrections: 2

MESSAGE SUMMARY

203 E: 1 (No. of Seq. differs)

252 E: 1 (No. of Seq. differs)

259 W: 49 (Allowed number of lines exceeded)

270 C: 1 (Current Application Number differs)

271 C: 1 (Current Filing Date differs)

283 W: 3 (Missing Blank Line separator)